

SEQUENCE LISTING

<110> Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.

<120> Immunokinases

<130> 042950wo Me/FM

<140> PCT/EP2005/050131

<141> 2005-01-13

<150> 04000847.6

<151> 2004-01-16

<150> 04017928.5

<151> 2004-07-29

<160> 9

<170> PatentIn Ver. 2.1

<210> 1

<211> 1785

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

pMS-(L-DAPK2'-Ki-4)-III/G open reading frame (ORF)

<220>

<221> CDS

<222> (1)..(1785)

<220>

<221> N_region

<222> (1)..(21)

<223> immunoglobulin kappa chain leader sequence

<400> 1

atg	gag	aca	gac	aca	ctc	ctg	cta	tgg	gta	ctg	ctg	ctc	tgg	gtt	cca	48
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1				5				10					15			

ggt	tcc	act	ggt	gac	tct	aga	atg	gtc	cag	gcc	tcg	atg	agg	agc	cca	96
Gly	Ser	Thr	Gly	Asp	Ser	Arg	Met	Val	Gln	Ala	Ser	Met	Arg	Ser	Pro	
			20					25					30			

aat	atg	gag	acg	ttc	aaa	cag	cag	aag	gtg	gag	gac	ttt	tat	gat	att	144
Asn	Met	Glu	Thr	Phe	Lys	Gln	Gln	Lys	Val	Glu	Asp	Phe	Tyr	Asp	Ile	
		35				40					45					

gga	gag	gag	ctg	ggc	agt	ggc	cag	ttt	gcc	atc	gtg	aag	aag	tgc	cgg	192
Gly	Glu	Glu	Leu	Gly	Ser	Gly	Gln	Phe	Ala	Ile	Val	Lys	Lys	Cys	Arg	
	50					55					60					

gag	aag	agc	acg	ggg	ctg	gag	tat	gca	gcc	aag	ttc	att	aag	aag	agg	240
Glu	Lys	Ser	Thr	Gly	Leu	Glu	Tyr	Ala	Ala	Lys	Phe	Ile	Lys	Lys	Arg	
65					70					75					80	
cag	agc	cgg	gcc	agc	cgt	cgg	ggc	gtg	tgc	cgg	gag	gaa	atc	gag	cgg	288
Gln	Ser	Arg	Ala	Ser	Arg	Arg	Gly	Val	Cys	Arg	Glu	Glu	Ile	Glu	Arg	
				85					90						95	
gag	gtg	agc	atc	ctg	cgg	cag	gtg	ctg	cac	ccc	aac	atc	atc	acg	ctg	336
Glu	Val	Ser	Ile	Leu	Arg	Gln	Val	Leu	His	Pro	Asn	Ile	Ile	Thr	Leu	
			100					105						110		
cac	gac	gtc	tat	gag	aac	cgc	acc	gac	gtg	gtg	ctc	atc	ctt	gag	cta	384
His	Asp	Val	Tyr	Glu	Asn	Arg	Thr	Asp	Val	Val	Leu	Ile	Leu	Glu	Leu	
			115					120						125		
gtg	tcc	gga	gga	gaa	ctg	ttt	gat	ttc	ctg	gcc	cag	aag	gag	tcg	tta	432
Val	Ser	Gly	Gly	Glu	Leu	Phe	Asp	Phe	Leu	Ala	Gln	Lys	Glu	Ser	Leu	
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agt	gag	gag	gaa	gcc	acc	agc	ttc	att	aag	cag	atc	ctg	gat	ggg	gtg	480
Ser	Glu	Glu	Glu	Ala	Thr	Ser	Phe	Ile	Lys	Gln	Ile	Leu	Asp	Gly	Val	
145					150					155					160	
aat	tac	ctt	cac	aca	aag	aaa	att	gct	cac	ttt	gat	ctc	aag	cca	gaa	528
Asn	Tyr	Leu	His	Thr	Lys	Lys	Ile	Ala	His	Phe	Asp	Leu	Lys	Pro	Glu	
				165					170						175	
aac	atc	atg	ttg	tta	gac	aag	aat	atc	cca	att	cca	cac	atc	aag	ctg	576
Asn	Ile	Met	Leu	Leu	Asp	Lys	Asn	Ile	Pro	Ile	Pro	His	Ile	Lys	Leu	
				180					185					190		
att	gac	ttt	ggc	ctg	gct	cac	gaa	ata	gaa	gat	gga	gtt	gaa	ttt	aaa	624
Ile	Asp	Phe	Gly	Leu	Ala	His	Glu	Ile	Glu	Asp	Gly	Val	Glu	Phe	Lys	
			195					200					205			
aac	att	ttt	ggg	aca	cct	gaa	ttt	gtt	gct	cca	gaa	atc	gtg	aac	tat	672
Asn	Ile	Phe	Gly	Thr	Pro	Glu	Phe	Val	Ala	Pro	Glu	Ile	Val	Asn	Tyr	
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gag	cca	ctg	gga	ctg	gag	gcc	gac	atg	tgg	agc	att	gga	gtc	atc	acc	720
Glu	Pro	Leu	Gly	Leu	Glu	Ala	Asp	Met	Trp	Ser	Ile	Gly	Val	Ile	Thr	
225						230					235				240	
tat	atc	ctt	cta	agt	gga	gcg	tcc	ccc	ttc	ctg	gga	gac	aca	aaa	caa	768
Tyr	Ile	Leu	Leu	Ser	Gly	Ala	Ser	Pro	Phe	Leu	Gly	Asp	Thr	Lys	Gln	
				245					250						255	
gaa	acc	ctg	gca	aat	atc	act	gct	gtg	agt	tac	gac	ttt	gat	gag	gaa	816
Glu	Thr	Leu	Ala	Asn	Ile	Thr	Ala	Val	Ser	Tyr	Asp	Phe	Asp	Glu	Glu	
			260					265						270		
ttc	ttc	agc	cag	aca	agc	gag	ctg	gcc	aag	gac	ttc	att	cgg	aag	ctt	864
Phe	Phe	Ser	Gln	Thr	Ser	Glu	Leu	Ala	Lys	Asp	Phe	Ile	Arg	Lys	Leu	
		275					280					285				

ctt	gtg	aaa	gag	acc	cgg	aaa	cgg	ctt	acc	atc	caa	gag	gct	ctc	aga	912
Leu	Val	Lys	Glu	Thr	Arg	Lys	Arg	Leu	Thr	Ile	Gln	Glu	Ala	Leu	Arg	
	290						295					300				
cat	ccc	tgg	atc	gga	tcc	aaa	cta	gct	gag	cac	gaa	ggg	gac	gcg	gcc	960
His	Pro	Trp	Ile	Gly	Ser	Lys	Leu	Ala	Glu	His	Glu	Gly	Asp	Ala	Ala	
	305					310				315					320	
cag	ccg	gcc	atg	gcc	cag	gtc	aag	ctg	cag	gag	tca	ggg	act	gaa	ctg	1008
Gln	Pro	Ala	Met	Ala	Gln	Val	Lys	Leu	Gln	Glu	Ser	Gly	Thr	Glu	Leu	
				325					330					335		
gca	aag	cct	ggg	gcc	gca	gtg	aag	atg	tcc	tgc	aag	gct	tct	ggc	tac	1056
Ala	Lys	Pro	Gly	Ala	Ala	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	
			340					345					350			
acc	ttt	act	gac	tac	tgg	atg	cac	tgg	gtt	aaa	cag	agg	cct	gga	cag	1104
Thr	Phe	Thr	Asp	Tyr	Trp	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	
		355					360					365				
ggg	ctg	gaa	tgg	att	gga	tac	att	aat	cct	aac	act	gct	tat	act	gac	1152
Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn	Pro	Asn	Thr	Ala	Tyr	Thr	Asp	
	370					375					380					
tac	aat	cag	aaa	ttc	aag	gac	aag	gcc	aca	ttg	act	gca	gac	aaa	tcc	1200
Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	
	385				390					395					400	
tcc	agc	aca	gcc	tac	atg	caa	ctg	cgc	agc	ctg	acc	tct	gag	gat	tct	1248
Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	
			405					410					415			
gca	gtc	tat	tac	tgt	gca	aaa	aag	aca	act	cag	act	acg	tgg	ggg	ttt	1296
Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Lys	Thr	Thr	Gln	Thr	Thr	Trp	Gly	Phe	
			420					425					430			
cct	ttt	tgg	ggc	caa	ggg	acc	acg	gtc	acc	gtc	tcc	tca	ggg	gga	ggc	1344
Pro	Phe	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	
		435					440				445					
ggg	tca	ggc	gga	ggg	ggc	tct	ggc	ggg	ggc	gga	tgc	gac	att	gtg	ctg	1392
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Val	Leu	
	450					455					460					
acc	cag	tct	cca	aaa	tcc	atg	gcc	atg	tca	gtc	gga	gag	agg	gtc	acc	1440
Thr	Gln	Ser	Pro	Lys	Ser	Met	Ala	Met	Ser	Val	Gly	Glu	Arg	Val	Thr	
	465				470				475						480	
ttg	agc	tgc	aag	gcc	agt	gag	aat	gtg	gat	tct	ttt	gtt	tcc	tgg	tat	1488
Leu	Ser	Cys	Lys	Ala	Ser	Glu	Asn	Val	Asp	Ser	Phe	Val	Ser	Trp	Tyr	
			485					490						495		
caa	cag	aaa	cca	ggc	cag	tct	cct	aaa	ctg	ctg	ata	tac	ggg	gcc	tcc	1536
Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Gly	Ala	Ser	
			500					505					510			

aac cgg tac act ggg gtc ccc gat cgc ttc gca ggc agt gga tct gga	1584
Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly Ser Gly	
515 520 525	
aga gat ttc act ctg acc atc agc agt gtg cag gct gaa gac ctt gca	1632
Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala	
530 535 540	
gat tat cac tgt gga cag aat tac agg tat ccg ctc acg ttc ggt gct	1680
Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe Gly Ala	
545 550 555 560	
ggc acc aag ctg gaa atc aaa cgg gcg gcc gca ggg ccc gaa caa aaa	1728
Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Gly Pro Glu Gln Lys	
565 570 575	
ctc atc tca gaa gag gat ctg aat agc gcc gtc gac cat cat cat cat	1776
Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His	
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His His	
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<210> 2

<211> 594

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence:

pMS-(L-DAPK2'-Ki-4)-III/G open reading frame (ORF)

<400> 2

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Asn Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile	
35 40 45	
Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg	
50 55 60	
Glu Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg	
65 70 75 80	
Gln Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg	
85 90 95	
Glu Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu	
100 105 110	
His Asp Val Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu	
115 120 125	
Val Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu	
130 135 140	
Ser Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val	
145 150 155 160	
Asn Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu	
165 170 175	
Asn Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu	

Ile	Asp	Phe	Gly	Leu	Ala	His	Glu	Ile	Glu	Asp	Gly	Val	Glu	Phe	Lys
		180						185					190		
Asn	Ile	Phe	Gly	Thr	Pro	Glu	Phe	Val	Ala	Pro	Glu	Ile	Val	Asn	Tyr
		195						200					205		
Glu	Pro	Leu	Gly	Leu	Glu	Ala	Asp	Met	Trp	Ser	Ile	Gly	Val	Ile	Thr
		210						215					220		
Tyr	Ile	Leu	Leu	Ser	Gly	Ala	Ser	Pro	Phe	Leu	Gly	Asp	Thr	Lys	Gln
Glu	Thr	Leu	Ala	Asn	Ile	Thr	Ala	Val	Ser	Tyr	Asp	Phe	Asp	Glu	Glu
Phe	Phe	Ser	Gln	Thr	Ser	Glu	Leu	Ala	Lys	Asp	Phe	Ile	Arg	Lys	Leu
Leu	Val	Lys	Glu	Thr	Arg	Lys	Arg	Leu	Thr	Ile	Gln	Glu	Ala	Leu	Arg
His	Pro	Trp	Ile	Gly	Ser	Lys	Leu	Ala	Glu	His	Glu	Gly	Asp	Ala	Ala
Gln	Pro	Ala	Met	Ala	Gln	Val	Lys	Leu	Gln	Glu	Ser	Gly	Thr	Glu	Leu
Ala	Lys	Pro	Gly	Ala	Ala	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr
Thr	Phe	Thr	Asp	Tyr	Trp	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln
Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn	Pro	Asn	Thr	Ala	Tyr	Thr	Asp
Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser
Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser
Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Lys	Thr	Thr	Gln	Thr	Thr	Trp	Gly	Phe
Pro	Phe	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Val	Leu
Thr	Gln	Ser	Pro	Lys	Ser	Met	Ala	Met	Ser	Val	Gly	Glu	Arg	Val	Thr
Leu	Ser	Cys	Lys	Ala	Ser	Glu	Asn	Val	Asp	Ser	Phe	Val	Ser	Trp	Tyr
Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Gly	Ala	Ser
Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Ala	Gly	Ser	Gly	Ser	Gly
Arg	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala
Asp	Tyr	His	Cys	Gly	Gln	Asn	Tyr	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Ala
Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Gly	Pro	Glu	Gln	Lys
Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Ser	Ala	Val	Asp	His	His	His	His
His	His														

<211> 1794

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

pMS-(Ki-4-DAPK2')-II/G ORF

<220>

<221> CDS

<222> (1)..(1794)

<220>

<221> N_region

<222> (1)..(21)

<223> immunoglobulin kappa chain leader sequence

<400> 3

atg gag aca gac aca ctc ctg cta tgg gta ctg ctg ctc tgg gtt cca	48
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro	
1 5 10 15	
ggt tcc act ggt gac gcg gcc cag ccg gcc atg gcc cag gtc aag ctg	96
Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu	
20 25 30	
cag gag tca ggg act gaa ctg gca aag cct ggg gcc gca gtg aag atg	144
Gln Glu Ser Gly Thr Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met	
35 40 45	
tcc tgc aag gct tct ggc tac acc ttt act gac tac tgg atg cac tgg	192
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp	
50 55 60	
gtt aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att aat	240
Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn	
65 70 75 80	
cct aac act gct tat act gac tac aat cag aaa ttc aag gac aag gcc	288
Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala	
85 90 95	
aca ttg act gca gac aaa tcc tcc agc aca gcc tac atg caa ctg cgc	336
Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg	
100 105 110	
agc ctg acc tct gag gat tct gca gtc tat tac tgt gca aaa aag aca	384
Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr	
115 120 125	
act cag act acg tgg ggg ttt cct ttt tgg ggc caa ggg acc acg gtc	432
Thr Gln Thr Thr Trp Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val	
130 135 140	
acc gtc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct ggc ggt	480
Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	

145	150							155							160					
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gat Asp	tct Ser	ttt Phe 195	gtt Val	tcc Ser	tgg Trp	tat Tyr	caa Gln 200	cag Gln	aaa Lys	cca Pro	ggc Gly	cag Gln 205	tct Ser	cct Pro	aaa Lys	624				
ctg Leu	ctg Leu 210	ata Ile	tac Tyr	ggg Gly	gcc Ala	tcc Ser 215	aac Asn	cgg Arg	tac Tyr	act Thr	ggg Gly 220	gtc Val	ccc Pro	gat Asp	cgc Arg	672				
ttc Phe 225	gca Ala	ggc Gly	agt Ser	gga Gly 230	tct Ser	gga Gly	aga Arg	gat Asp	ttc Phe 235	act Thr	ctg Leu	acc Thr	atc Ile	agc Ser	agt Ser 240	720				
gtg Val	cag Gln	gct Ala	gaa Glu 245	gac Asp	ctt Leu	gca Ala	gat Asp	tat Tyr	cac His 250	tgt Cys	gga Gly	cag Gln	aat Asn	tac Tyr 255	agg Arg	768				
tat Tyr	ccg Pro	ctc Leu	acg Thr 260	ttc Phe	ggg Gly	gct Ala	ggc Gly	acc Thr 265	aag Lys	ctg Leu	gaa Glu	atc Ile	aaa Lys 270	cgg Arg	gcg Ala	816				
gcc Ala	gca Ala	ctc Leu 275	gag Glu	tct Ser	aga Arg	atg Met	gtc Val 280	cag Gln	gcc Ala	tcg Ser	atg Met	agg Arg 285	agc Ser	cca Pro	aat Asn	864				
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gag Glu 305	gag Glu	ctg Leu	ggc Gly	agt Ser	ggc Gly 310	cag Gln	ttt Phe	gcc Ala	atc Ile	gtg Val 315	aag Lys	aag Lys	tgc Cys	cgg Arg	gag Glu 320	960				
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agc Ser	cgg Arg	gcc Ala	agc Ser 340	cgt Arg	cgg Arg	ggc Gly	gtg Val	tgc Cys 345	cgg Arg	gag Glu	gaa Glu	atc Ile	gag Glu 350	cgg Arg	gag Glu	1056				
gtg Val	agc Ser	atc Ile 355	ctg Leu	cgg Arg	cag Gln	gtg Val	ctg Leu 360	cac His	ccc Pro	aac Asn	atc Ile	atc Ile 365	acg Thr	ctg Leu	cac His	1104				
gac Asp	ctc Leu	tat Tyr	gag Glu	aac Asn	cgc Arg	acc Thr	gac Asp	gtg Val	gtg Val	ctc Leu	atc Ile	ctt Leu	gag Glu	cta Leu	gtg Val	1152				

370	375	380	
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gag gag gaa gcc acc agc ttc att aag cag atc ctg gat ggg gtg aat Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val Asn 405 410 415			1248
tac ctt cac aca aag aaa att gct cac ttt gat ctc aag cca gaa aac Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn 420 425 430			1296
atc atg ttg tta gac aag aat atc cca att cca cac atc aag ctg att Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu Ile 435 440 445			1344
gac ttt ggc ctg gct cac gaa ata gaa gat gga gtt gaa ttt aaa aac Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys Asn 450 455 460			1392
att ttt ggg aca cct gaa ttt gtt gct cca gaa atc gtg aac tat gag Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu 465 470 475 480			1440
cca ctg gga ctg gag gcc gac atg tgg agc att gga gtc atc acc tat Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr 485 490 495			1488
atc ctt cta agt gga gcg tcc ccc ttc ctg gga gac aca aaa caa gaa Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu 500 505 510			1536
acc ctg gca aat atc act gct gtg agt tac gac ttt gat gag gaa ttc Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu Phe 515 520 525			1584
ttc agc cag aca agc gag ctg gcc aag gac ttc att cgg aag ctt ctt Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu 530 535 540			1632
gtg aaa gag acc cgg aaa cgg ctt acc atc caa gag gct ctc aga cat Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His 545 550 555 560			1680
ccc tgg atc gga tcc aaa cta gct gag cac gaa ttt cga gga ggg ccc Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Phe Arg Gly Gly Pro 565 570 575			1728
gaa caa aaa ctc atc tca gaa gag gat ctg aat agc gcc gtc gac cat Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His 580 585 590			1776
cat cat cat cat cat tga His His His His His			1794

595

<210> 4
 <211> 597
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:
 pMS-(Ki-4-DAPK2')-II/G ORF

<400> 4
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 Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu
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 Gln Glu Ser Gly Thr Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met
 35 40 45
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp
 50 55 60
 Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 65 70 75 80
 Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala
 85 90 95
 Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg
 100 105 110
 Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr
 115 120 125
 Thr Gln Thr Thr Trp Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val
 130 135 140
 Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 145 150 155 160
 Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met
 165 170 175
 Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val
 180 185 190
 Asp Ser Phe Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
 195 200 205
 Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
 210 215 220
 Phe Ala Gly Ser Gly Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser
 225 230 235 240
 Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg
 245 250 255
 Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala
 260 265 270
 Ala Ala Leu Glu Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro Asn
 275 280 285
 Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly
 290 295 300
 Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu
 305 310 315 320
 Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Gln
 325 330 335
 Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg Glu
 340 345 350
 Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu His

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      355      360      365
Asp Leu Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu Val
  370      375      380
Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu Ser
385      390      395      400
Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val Asn
      405      410      415
Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn
      420      425      430
Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu Ile
      435      440      445
Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys Asn
      450      455      460
Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu
465      470      475      480
Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr
      485      490      495
Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu
      500      505      510
Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu Phe
      515      520      525
Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu
      530      535      540
Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His
545      550      555      560
Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Phe Arg Gly Gly Pro
      565      570      575
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His
      580      585      590
His His His His His
      595

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<210> 5

<211> 3102

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pMT-Ki-4
(scFv)-eEF-2K ORF

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<221> CDS

<222> (1)..(3102)

<220>

<221> N_region

<222> (2)..(22)

<223> pelB leader sequence

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gcc cag ccg gcg atg gcc atg ggc cat cat cat cat cat cat cat cat	96
Ala Gln Pro Ala Met Ala Met Gly His His His His His His His His	
20 25 30	
cat cac agc agc ggc cat atc gac gac gac gac aag cat atg aag ctt	144
His His Ser Ser Gly His Ile Asp Asp Asp Asp Lys His Met Lys Leu	
35 40 45	
atg gcc cag ccg gcc atg gcc cag gtc aag ctg cag gag tca ggg act	192
Met Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr	
50 55 60	
gaa ctg gca aag cct ggg gcc gca gtg aag atg tcc tgc aag gct tct	240
Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser	
65 70 75 80	
ggc tac acc ttt act gac tac tgg atg cac tgg gtt aaa cag agg cct	288
Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro	
85 90 95	
gga cag ggt ctg gaa tgg att gga tac att aat cct aac act gct tat	336
Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr	
100 105 110	
act gac tac aat cag aaa ttc aag gac aag gcc aca ttg act gca gac	384
Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp	
115 120 125	
aaa tcc tcc agc aca gcc tac atg caa ctg cgc agc ctg acc tct gag	432
Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu	
130 135 140	
gat tct gca gtc tat tac tgt gca aaa aag aca act cag act acg tgg	480
Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp	
145 150 155 160	
ggg ttt cct ttt tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt	528
Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly	
165 170 175	
gga ggc ggt tca ggc gga ggt ggc tct ggc ggt ggc gga tgc gac att	576
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile	
180 185 190	
gtg ctg acc cag tct cca aaa tcc atg gcc atg tca gtc gga gag agg	624
Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg	
195 200 205	
gtc acc ttg agc tgc aag gcc agt gag aat gtg gat tct ttt gtt tcc	672
Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser	
210 215 220	
tgg tat caa cag aaa cca ggc cag tct cct aaa ctg ctg ata tac ggg	720
Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly	
225 230 235 240	

gcc tcc aac cgg tac act ggg gtc ccc gat cgc ttc gca ggc agt gga Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly 245 250 255	768
tct gga aga gat ttc act ctg acc atc agc agt gtg cag gct gaa gac Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp 260 265 270	816
ctt gca gat tat cac tgt gga cag aat tac agg tat ccg ctc acg ttc Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe 275 280 285	864
ggc gct ggc acc aag ctg gaa atc aaa cgg gcg gcc gca gag ctc ggc Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu Leu Gly 290 295 300	912
gga ggt ggc tct atg gca gac gaa gat ctc atc ttc cgc ctg gaa ggc Gly Gly Gly Ser Met Ala Asp Glu Asp Leu Ile Phe Arg Leu Glu Gly 305 310 315 320	960
gtt gat ggc ggc cag tcc ccc cga gct ggc cat gat ggt gat tct gat Val Asp Gly Gly Gln Ser Pro Arg Ala Gly His Asp Gly Asp Ser Asp 325 330 335	1008
ggg gac agc gac gat gag gaa ggt tac ttc atc tgc ccc atc acg gat Gly Asp Ser Asp Asp Glu Glu Gly Tyr Phe Ile Cys Pro Ile Thr Asp 340 345 350	1056
gac cca agc tcg aac cag aat gtc aat tcc aag gtt aat aag tac tac Asp Pro Ser Ser Asn Gln Asn Val Asn Ser Lys Val Asn Lys Tyr Tyr 355 360 365	1104
agc aac cta aca aaa agt gag cgg tat agc tcc agc ggg tcc ccg gca Ser Asn Leu Thr Lys Ser Glu Arg Tyr Ser Ser Ser Gly Ser Pro Ala 370 375 380	1152
aac tcc ttc cac ttc aag gaa gcc tgg aag cac gca atc cag aag gcc Asn Ser Phe His Phe Lys Glu Ala Trp Lys His Ala Ile Gln Lys Ala 385 390 395 400	1200
aag cac atg ccc gac ccc tgg gct gag ttc cac ctg gaa gat att gcc Lys His Met Pro Asp Pro Trp Ala Glu Phe His Leu Glu Asp Ile Ala 405 410 415	1248
acc gaa cgt gct act cga cac agg tac aac gcc gtc acc ggg gaa tgg Thr Glu Arg Ala Thr Arg His Arg Tyr Asn Ala Val Thr Gly Glu Trp 420 425 430	1296
ctg gat gat gaa gtt ctg atc aag atg gca tct cag ccc ttc ggc cga Leu Asp Asp Glu Val Leu Ile Lys Met Ala Ser Gln Pro Phe Gly Arg 435 440 445	1344
gga gca atg agg gag tgc ttc cgg acg aag aag ctc tcc aac ttc ttg Gly Ala Met Arg Glu Cys Phe Arg Thr Lys Lys Leu Ser Asn Phe Leu 450 455 460	1392

cat gcc cag cag tgg aag ggc gcc tcc aac tac gtg gcg aag cgc tac	1440
His Ala Gln Gln Trp Lys Gly Ala Ser Asn Tyr Val Ala Lys Arg Tyr	
465 470 475 480	
atc gag ccc gta gac cgg gat gtg tac ttt gag gac gtg cgt cta cag	1488
Ile Glu Pro Val Asp Arg Asp Val Tyr Phe Glu Asp Val Arg Leu Gln	
485 490 495	
atg gag gcc aag ctc tgg ggg gag gag tat aat cgg cac aag ccc ccc	1536
Met Glu Ala Lys Leu Trp Gly Glu Glu Tyr Asn Arg His Lys Pro Pro	
500 505 510	
aag cag gtg gac atc atg cag atg tgc atc atc gag ctg aag gac aga	1584
Lys Gln Val Asp Ile Met Gln Met Cys Ile Ile Glu Leu Lys Asp Arg	
515 520 525	
ccg ggc aag ccc ctc ttc cac ctg gag cac tac atc gag ggc aag tac	1632
Pro Gly Lys Pro Leu Phe His Leu Glu His Tyr Ile Glu Gly Lys Tyr	
530 535 540	
atc aag tac aac tcc aac tct ggc ttt gtc cgc gat gac aac atc cgc	1680
Ile Lys Tyr Asn Ser Asn Ser Gly Phe Val Arg Asp Asp Asn Ile Arg	
545 550 555 560	
ctg acg ccg cag gcc ttc agc cac ttc act ttt gag cgt tcc ggc cat	1728
Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg Ser Gly His	
565 570 575	
cag ctg ata gtg gtg gac atc cag gga gtt ggg gat ctc tac act gac	1776
Gln Leu Ile Val Val Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp	
580 585 590	
cca cag atc cac acg gag acg ggc act gac ttt gga gac ggc aac cta	1824
Pro Gln Ile His Thr Glu Thr Gly Thr Asp Phe Gly Asp Gly Asn Leu	
595 600 605	
ggg gtc cgc ggg atg gcg ctc ttc ttc tac tct cat gcc tgc aac cgg	1872
Gly Val Arg Gly Met Ala Leu Phe Phe Tyr Ser His Ala Cys Asn Arg	
610 615 620	
att tgc gag agc atg ggc ctt gct ccc ttt gac ctc tcg ccc cgg gag	1920
Ile Cys Glu Ser Met Gly Leu Ala Pro Phe Asp Leu Ser Pro Arg Glu	
625 630 635 640	
agg gat gca gtg aat cag aac acc aag ctg ctg caa tca gcc aag acc	1968
Arg Asp Ala Val Asn Gln Asn Thr Lys Leu Leu Gln Ser Ala Lys Thr	
645 650 655	
atc ttg aga gga aca gag gaa aaa tgt ggg agc ccc cga gta agg acc	2016
Ile Leu Arg Gly Thr Glu Glu Lys Cys Gly Ser Pro Arg Val Arg Thr	
660 665 670	
ctc tct ggg agc cgg cca ccc ctg ctc cgt ccc ctt tca gag aac tct	2064
Leu Ser Gly Ser Arg Pro Pro Leu Leu Arg Pro Leu Ser Glu Asn Ser	
675 680 685	

gga gac gag aac atg agc gac gtg acc ttc gac tct ctc cct tct tcc	2112
Gly Asp Glu Asn Met Ser Asp Val Thr Phe Asp Ser Leu Pro Ser Ser	
690 695 700	
cca tct tcg gcc aca cca cac agc cag aag cta gac cac ctc cat tgg	2160
Pro Ser Ser Ala Thr Pro His Ser Gln Lys Leu Asp His Leu His Trp	
705 710 715 720	
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Pro Val Phe Ser Asp Leu Asp Asn Met Ala Ser Arg Asp His Asp His	
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cta gac aac cac cgg gag tct gag aat agt ggg gac agc gga tac ccc	2256
Leu Asp Asn His Arg Glu Ser Glu Asn Ser Gly Asp Ser Gly Tyr Pro	
740 745 750	
agt gag aag cgg ggt gag ctg gat gac cct gag ccc cga gaa cat ggc	2304
Ser Glu Lys Arg Gly Glu Leu Asp Asp Pro Glu Pro Arg Glu His Gly	
755 760 765	
cac tca tac agt aat cgg aag tac gag tct gac gaa gac agc ctg ggc	2352
His Ser Tyr Ser Asn Arg Lys Tyr Glu Ser Asp Glu Asp Ser Leu Gly	
770 775 780	
agc tct gga cgg gta tgt gta gag aag tgg aat ctc ctc aac tcc tcc	2400
Ser Ser Gly Arg Val Cys Val Glu Lys Trp Asn Leu Leu Asn Ser Ser	
785 790 795 800	
cgc ctc cac ctg ccg agg gct tcg gcc gtg gcc ctg gaa gtg caa agg	2448
Arg Leu His Leu Pro Arg Ala Ser Ala Val Ala Leu Glu Val Gln Arg	
805 810 815	
ctt aat gct ctg gac ctc gaa aag aaa atc ggg aag tcc att ttg ggg	2496
Leu Asn Ala Leu Asp Leu Glu Lys Lys Ile Gly Lys Ser Ile Leu Gly	
820 825 830	
aag gtc cat ctg gcc atg gtg cgc tac cac gag ggt ggg cgc ttc tgc	2544
Lys Val His Leu Ala Met Val Arg Tyr His Glu Gly Gly Arg Phe Cys	
835 840 845	
gag aag ggc gag gag tgg gac cag gag tcg gct gtc ttc cac ctg gag	2592
Glu Lys Gly Glu Glu Trp Asp Gln Glu Ser Ala Val Phe His Leu Glu	
850 855 860	
cac gca gcc aac ctg ggc gag ctg gag gcc atc gtg ggc ctg gga ctc	2640
His Ala Ala Asn Leu Gly Glu Leu Glu Ala Ile Val Gly Leu Gly Leu	
865 870 875 880	
atg tac tcg cag ttg cct cat cac atc cta gcc gat gtc tct ctg aag	2688
Met Tyr Ser Gln Leu Pro His His Ile Leu Ala Asp Val Ser Leu Lys	
885 890 895	
gag aca gaa gag aac aaa acc aaa gga ttt gat tac tta cta aag gcc	2736
Glu Thr Glu Glu Asn Lys Thr Lys Gly Phe Asp Tyr Leu Leu Lys Ala	
900 905 910	

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gct gaa gct ggc gac agg cag tcc atg atc cta gtg gcg cga gct ttt 2784
Ala Glu Ala Gly Asp Arg Gln Ser Met Ile Leu Val Ala Arg Ala Phe
      915                      920                      925

gac tct ggc cag aac ctc agc ccg gac agg tgc caa gac tgg cta gag 2832
Asp Ser Gly Gln Asn Leu Ser Pro Asp Arg Cys Gln Asp Trp Leu Glu
      930                      935                      940

gcc ctg cac tgg tac aac act gcc ctg gag atg acg gac tgt gat gag 2880
Ala Leu His Trp Tyr Asn Thr Ala Leu Glu Met Thr Asp Cys Asp Glu
      945                      950                      955                      960

ggc ggt gag tac gac gga atg cag gac gag ccc cgg tac atg atg ctg 2928
Gly Gly Glu Tyr Asp Gly Met Gln Asp Glu Pro Arg Tyr Met Met Leu
      965                      970                      975

gcc agg gag gcc gag atg ctg ttc aca gga ggc tac ggg ctg gag aag 2976
Ala Arg Glu Ala Glu Met Leu Phe Thr Gly Gly Tyr Gly Leu Glu Lys
      980                      985                      990

gac ccg cag aga tca ggg gac ttg tat acc cag gca gca gag gca gcg 3024
Asp Pro Gln Arg Ser Gly Asp Leu Tyr Thr Gln Ala Ala Glu Ala Ala
      995                      1000                      1005

atg gaa gcc atg aag ggc cga ctg gcc aac cag tac tac caa aag gct 3072
Met Glu Ala Met Lys Gly Arg Leu Ala Asn Gln Tyr Tyr Gln Lys Ala
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gaa gag gcc tgg gcc cag atg gag gag taa 3102
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<211> 1033

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pMT-Ki-4
(scFv)-eEF-2K ORF

<400> 6

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Ala Gln Pro Ala Met Ala Met Gly His His His His His His His
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His His Ser Ser Gly His Ile Asp Asp Asp Lys His Met Lys Leu
      35              40              45
Met Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr
      50              55              60
Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser
      65              70              75              80
Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro
      85              90              95
Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr
      100              105              110

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Thr	Asp	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Ala	Asp
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Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Arg	Ser	Leu	Thr	Ser	Glu
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Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Lys	Thr	Thr	Gln	Thr	Thr	Trp
145					150					155					160
Gly	Phe	Pro	Phe	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly
			165					170						175	
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile
			180					185					190		
Val	Leu	Thr	Gln	Ser	Pro	Lys	Ser	Met	Ala	Met	Ser	Val	Gly	Glu	Arg
		195					200					205			
Val	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Glu	Asn	Val	Asp	Ser	Phe	Val	Ser
		210				215					220				
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Gly
225					230					235					240
Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Ala	Gly	Ser	Gly
			245					250						255	
Ser	Gly	Arg	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp
			260					265					270		
Leu	Ala	Asp	Tyr	His	Cys	Gly	Gln	Asn	Tyr	Arg	Tyr	Pro	Leu	Thr	Phe
		275					280					285			
Gly	Ala	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Glu	Leu	Gly
		290				295				300					
Gly	Gly	Gly	Ser	Met	Ala	Asp	Glu	Asp	Leu	Ile	Phe	Arg	Leu	Glu	Gly
305					310				315						320
Val	Asp	Gly	Gly	Gln	Ser	Pro	Arg	Ala	Gly	His	Asp	Gly	Asp	Ser	Asp
				325					330					335	
Gly	Asp	Ser	Asp	Asp	Glu	Glu	Gly	Tyr	Phe	Ile	Cys	Pro	Ile	Thr	Asp
			340					345					350		
Asp	Pro	Ser	Ser	Asn	Gln	Asn	Val	Asn	Ser	Lys	Val	Asn	Lys	Tyr	Tyr
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Ser	Asn	Leu	Thr	Lys	Ser	Glu	Arg	Tyr	Ser	Ser	Ser	Gly	Ser	Pro	Ala
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Asn	Ser	Phe	His	Phe	Lys	Glu	Ala	Trp	Lys	His	Ala	Ile	Gln	Lys	Ala
385					390					395					400
Lys	His	Met	Pro	Asp	Pro	Trp	Ala	Glu	Phe	His	Leu	Glu	Asp	Ile	Ala
				405					410					415	
Thr	Glu	Arg	Ala	Thr	Arg	His	Arg	Tyr	Asn	Ala	Val	Thr	Gly	Glu	Trp
			420					425					430		
Leu	Asp	Asp	Glu	Val	Leu	Ile	Lys	Met	Ala	Ser	Gln	Pro	Phe	Gly	Arg
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Gly	Ala	Met	Arg	Glu	Cys	Phe	Arg	Thr	Lys	Lys	Leu	Ser	Asn	Phe	Leu
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His	Ala	Gln	Gln	Trp	Lys	Gly	Ala	Ser	Asn	Tyr	Val	Ala	Lys	Arg	Tyr
465					470					475					480
Ile	Glu	Pro	Val	Asp	Arg	Asp	Val	Tyr	Phe	Glu	Asp	Val	Arg	Leu	Gln
				485					490					495	
Met	Glu	Ala	Lys	Leu	Trp	Gly	Glu	Glu	Tyr	Asn	Arg	His	Lys	Pro	Pro
			500					505					510		
Lys	Gln	Val	Asp	Ile	Met	Gln	Met	Cys	Ile	Ile	Glu	Leu	Lys	Asp	Arg
		515					520					525			
Pro	Gly	Lys	Pro	Leu	Phe	His	Leu	Glu	His	Tyr	Ile	Glu	Gly	Lys	Tyr
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Ile	Lys	Tyr	Asn	Ser	Asn	Ser	Gly	Phe	Val	Arg	Asp	Asp	Asn	Ile	Arg
545					550					555					560

Leu	Thr	Pro	Gln	Ala	Phe	Ser	His	Phe	Thr	Phe	Glu	Arg	Ser	Gly	His
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Gln	Leu	Ile	Val	Val	Asp	Ile	Gln	Gly	Val	Gly	Asp	Leu	Tyr	Thr	Asp
			580					585					590		
Pro	Gln	Ile	His	Thr	Glu	Thr	Gly	Thr	Asp	Phe	Gly	Asp	Gly	Asn	Leu
		595					600					605			
Gly	Val	Arg	Gly	Met	Ala	Leu	Phe	Phe	Tyr	Ser	His	Ala	Cys	Asn	Arg
	610					615					620				
Ile	Cys	Glu	Ser	Met	Gly	Leu	Ala	Pro	Phe	Asp	Leu	Ser	Pro	Arg	Glu
625					630					635					640
Arg	Asp	Ala	Val	Asn	Gln	Asn	Thr	Lys	Leu	Leu	Gln	Ser	Ala	Lys	Thr
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Ile	Leu	Arg	Gly	Thr	Glu	Glu	Lys	Cys	Gly	Ser	Pro	Arg	Val	Arg	Thr
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Leu	Ser	Gly	Ser	Arg	Pro	Pro	Leu	Leu	Arg	Pro	Leu	Ser	Glu	Asn	Ser
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Gly	Asp	Glu	Asn	Met	Ser	Asp	Val	Thr	Phe	Asp	Ser	Leu	Pro	Ser	Ser
	690					695					700				
Pro	Ser	Ser	Ala	Thr	Pro	His	Ser	Gln	Lys	Leu	Asp	His	Leu	His	Trp
705					710					715					720
Pro	Val	Phe	Ser	Asp	Leu	Asp	Asn	Met	Ala	Ser	Arg	Asp	His	Asp	His
				725					730					735	
Leu	Asp	Asn	His	Arg	Glu	Ser	Glu	Asn	Ser	Gly	Asp	Ser	Gly	Tyr	Pro
			740					745					750		
Ser	Glu	Lys	Arg	Gly	Glu	Leu	Asp	Asp	Pro	Glu	Pro	Arg	Glu	His	Gly
		755					760					765			
His	Ser	Tyr	Ser	Asn	Arg	Lys	Tyr	Glu	Ser	Asp	Glu	Asp	Ser	Leu	Gly
	770					775				780					
Ser	Ser	Gly	Arg	Val	Cys	Val	Glu	Lys	Trp	Asn	Leu	Leu	Asn	Ser	Ser
785					790					795					800
Arg	Leu	His	Leu	Pro	Arg	Ala	Ser	Ala	Val	Ala	Leu	Glu	Val	Gln	Arg
				805					810					815	
Leu	Asn	Ala	Leu	Asp	Leu	Glu	Lys	Lys	Ile	Gly	Lys	Ser	Ile	Leu	Gly
		820						825					830		
Lys	Val	His	Leu	Ala	Met	Val	Arg	Tyr	His	Glu	Gly	Gly	Arg	Phe	Cys
		835					840					845			
Glu	Lys	Gly	Glu	Glu	Trp	Asp	Gln	Glu	Ser	Ala	Val	Phe	His	Leu	Glu
	850					855				860					
His	Ala	Ala	Asn	Leu	Gly	Glu	Leu	Glu	Ala	Ile	Val	Gly	Leu	Gly	Leu
865					870					875					880
Met	Tyr	Ser	Gln	Leu	Pro	His	His	Ile	Leu	Ala	Asp	Val	Ser	Leu	Lys
				885					890					895	
Glu	Thr	Glu	Glu	Asn	Lys	Thr	Lys	Gly	Phe	Asp	Tyr	Leu	Leu	Lys	Ala
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Ala	Glu	Ala	Gly	Asp	Arg	Gln	Ser	Met	Ile	Leu	Val	Ala	Arg	Ala	Phe
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Asp	Ser	Gly	Gln	Asn	Leu	Ser	Pro	Asp	Arg	Cys	Gln	Asp	Trp	Leu	Glu
	930					935					940				
Ala	Leu	His	Trp	Tyr	Asn	Thr	Ala	Leu	Glu	Met	Thr	Asp	Cys	Asp	Glu
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Gly	Gly	Glu	Tyr	Asp	Gly	Met	Gln	Asp	Glu	Pro	Arg	Tyr	Met	Met	Leu
				965					970					975	
Ala	Arg	Glu	Ala	Glu	Met	Leu	Phe	Thr	Gly	Gly	Tyr	Gly	Leu	Glu	Lys
			980					985					990		
Asp	Pro	Gln	Arg	Ser	Gly	Asp	Leu	Tyr	Thr	Gln	Ala	Ala	Glu	Ala	Ala
		995					1000						1005		

Met Glu Ala Met Lys Gly Arg Leu Ala Asn Gln Tyr Tyr Gln Lys Ala
1010 1015 1020
Glu Glu Ala Trp Ala Gln Met Glu Glu
1025 1030

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<212> PRT
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linker

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1 5 10 15

<210> 8
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1 5 10

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1 5